PESTKA-1-CIP

SUPER PROTEINS INCLUDING INTERFERONS, INTERLEUKINS, ET AL.

CROSS REFERENCE TO RELATED APPLICATION

This application is a continuation in part of copending U.S. application serial number 08/076,231, filed June 11, 1993.

FIELD OF THE INVENTION

This invention relates to the field of biotechnology and more particularly to polypeptides having antitumor, antiviral, immunomodulatory and other activities, DNA that codes for such polypeptides, recombinant vectors that include such DNA, host organisms transformed with the recombinant vector that produces the polypeptide and therapeutic application of the polypeptide.

The publications and other materials hereof used to illuminate the background of the invention, and in particular cases, to provide additional details respecting its practice are hereby incorporated by reference, and for convenience are numerically referenced by the following text and respectively grouped in the appended bibliography.

BACKGROUND OF THE INVENTION

Human leukocyte interferon was first discovered and prepared in the form of very crude fractions by Isaacs and Lindenmann (1, 2). Efforts to purify and characterize the material have led to the preparation of relatively homogeneous leukocyte interferons derived from normal or leukemic (chronic myelogenous leukemia or "CML") donors' leukocytes.

These interferons are a family of proteins characterized by a potent ability to confer a virus-resistant state in their target cells. In addition, interferon can inhibit cell proliferation, modulate immune responses and alter expression of proteins. These properties have prompted the clinical use of leukocyte interferon as a therapeutic agent for the treatment of viral infections and malignancies.

With the advent of recombinant DNA technology, the controlled microbial production of an enormous variety of useful polypeptides has become possible. The workhorse of recombinant DNA technology is the plasmid, a non-chromosomal circle of double-stranded DNA found in bacteria and other microbes, oftentimes in multiple copies per cell. Included in the information encoded in the plasmid DNA is that required to reproduce the plasmid (i.e., an origin of replication) and ordinarily, one or more selection characteristics such as, in the case of bacteria, resistance to antibiotics which permit clones of the host cell containing the plasmid of interest to be recognized and preferentially grown in selective media. The utility of plasmids lies in the fact that they can be specifically cleaved by one or another restriction endonuclease or "restriction enzyme," each of which recognizes a specific site in the DNA. Heterologous genes or gene fragments may be inserted into the plasmid at the cleavage site. To construct vectors with specific sequences inserted, DNA recombination is performed outside the cell, but the resulting "recombinant" plasmid can be introduced into cells by a process known as transformation and large quantities of the heterologous gene-containing recombinant plasmid obtained by growing the transformant. Moreover, where a promoter which governs the transcription of the encoded DNA message, is properly placed upstream (5') of a coding

sequence or a gene, the resulting expression vector can be used to produce the polypeptide sequence for which the inserted sequence or gene codes, a process referred to as expression.

Expression is initiated in a region known as the promoter which is recognized by and bound by RNA polymerase. In many cases promoter regions are overlapped by "control" regions such as the bacterial operators. Operators are DNA sequences which are recognized by so-called repressor proteins which serve to regulate the frequency of transcription initiation at a particular promoter. The polymerase travels along the DNA, transcribing the information contained in the coding strand from its 5' to 3' end into messenger RNA (mRNA) which is in turn translated into a polypeptide having the amino acid sequence for which the DNA codes. Each amino acid is encoded by a nucleotide triplet or "codon" within the coding sequence, i.e., that part which encodes the amino acid sequence of the expressed product. In bacteria (e.g. *Escherichia coli*) the mRNA contains a ribosome binding site, a translation initiation or "start" signal (ordinarily ATG in the DNA, which in the resulting mRNA becomes AUG), the nucleotide codons within the coding sequence itself, one or more stop codons, and an additional sequence of messenger RNA, the 3' untranslated region. Ribosomes bind to the binding site provided on the messenger RNA, in bacteria ordinarily as the mRNA is formed, and produce the encoded polypeptide, beginning at the translation start signal and ending at the stop signal. The desired product is produced if the sequences encoding the ribosome binding site are positioned properly with respect to the AUG initiator codon and if all remaining codons follow the initiator codon in phase. The resulting product may be obtained from the host cell and recovered by appropriate purification. In other systems, proteins may be secreted from the host cells. A wide variety of expression vectors

and host systems exist so that RNA and proteins may be expressed in prokaryotic and eukaryotic cells as well as in intact animals and plants.

During the past several decades a large number of human and animal interferons have been produced, identified, purified and cloned (see ref. 1-72). Several of the interferon preparations have been prepared for clinical trial in both crude form, for some of the original interferon preparations, as well as in purified form. Several individual recombinant interferon-α species have been cloned and expressed. The proteins have then been purified by various procedures and formulated for clinical use in a variety of formulations (73). Most of the interferons in clinical use that have been approved by various regulatory agencies throughout the world are mixtures or individual species of human α interferon (Hu-IFN-α). In some countries Hu-IFN-β and γ have also been approved for clinical trial and in some cases approved for therapeutic use (56,74). The major thesis underlying clinical use of these interferons was that they were natural molecules produced by normal individuals. Indeed, the specific thesis was that all the interferons prepared for clinical use, be they natural- or recombinant-generated products, represented interferons that were produced naturally by normal people. This is true for a large number of interferons as well as specific growth factors, lymphokines, cytokines, hormones, clotting factors and other proteins that have been produced (17, 21, 22, 25-27, 29-34, 39, 40, 45-51, 53-57, 62-64, 68-72).

Reports have suggested that Hu-IFN-αA (also designated Hu-IFN-α2a and by the trade name Roferon A) was not represented in interferons produced by a normal population of individuals (75-79). Believing that certain interferons (or, more generically, certain polypeptides) are uniquely found in diseased cells, the inventor of the present invention

undertook to identify interferons which are so uniquely characterized. For convenience the inventor began by screening known interferons, in particular, the sources of the several variants of Hu-IFN-α2 that have been described. As discussed more fully below, it was found that the source of two of the variants of Hu-IFN-α2, Hu-IFN-α2a and Hu-IFN-α2c, are not present in normal individuals. Only Hu-IFN-α2b is found in normal individuals (79).

DESCRIPTION OF THE DRAWINGS

Fig. 1. Nucleotide and Amino Acid Sequence of Hu-IFN-α001. The location of the *Alw*NI site is underlined. The signal peptide is shown as the 23 amino acids labeled -1 to -23.

Fig. 2. Comparison of the Protein Sequence of Hu-IFN-α001 with that of Hu-IFN-αJ. The signal peptide represents the first 23 amino acids at the amino terminus.

Fig. 3. Expression vector for Hu-IFN-α001. The structure of the plasmid pHu-IFN-α001 is shown. The *Nsi*I site represents nucleotide position #1. The P_R promoter drives expression of Hu-IFN-α001.

Fig. 4. SDS-Polyacrylamide Gel Electrophoresis of the Purified Hu-IFN-α001. Hu-IFN-α001 was placed in lanes 1, 2 and 3 in amounts of 3 μg, 1.5 μg and 0.75 μg, respectively. The columns labeled M represent the molecular weight markers with the values in kilodaltons given to the left of each respective molecular weight marker.

SUMMARY OF INVENTION

An extensive analysis of normal individuals from various ethnic and racial backgrounds as well as two tumor cell lines has shown that certain interferons originated from two cell lines that were obtained from patients with disease, in particular, malignancies of the hemopoietic system (79). These results lead the inventor to conclude that there is a new class of interferon molecules which are present in diseased states. specifically in tumors and blood borne malignancies. This discovery of a new class of interferons provides a wide variety of potentially new interferons for clinical and therapeutic use. These interferons include not only Hu-IFN-α species, but also Hu-IFN-β. Hu-IFN-γ and Hu-IFN-ω. as well as other newly described interferons in other animals and species. The observations suggest that growth factors, cytokines, lymphokines, clotting factors, peptide and polypeptide hormones, adhesion factors and many other molecules are also modified in disease processes. Therefore. modified forms of all these cytokines, lymphokines, growth factors, adhesion molecules, enzymes. clotting factors. peptide and polypeptide hormones. etc. will also occur in tumors and other diseases. Based on two presently identified members of this class (not previously recognized as such). these interferons are active. are as active as the standard molecules. and in fact have been used effectively for therapeutic purposes. A paper co-authored by the inventor and listed hereafter as Reference No. 79 is particularly related to the invention and is incorporated herein by reference insofar as may be needed for a full understanding of the invention. That paper is more fully described. and is furnished as an attachment to a contemporaneously filed Information Disclosure Statement.

DETAILED DESCRIPTION OF THE INVENTION

Four distinct classes of interferons (IFNs) are known to exist in humans. The IFN-α family represents the predominant class of IFNs and are produced by stimulated peripheral blood leukocytes (10-15, 17-27, 29, 50, 51, 57-59, 61, 63, 64, 68, 70), and lymphoblastoid and myeloblastoid cell lines (28, 30, 60). Cloning of the IFN-α genes from these cells has revealed that IFN-α is encoded by a multigene family consisting of about 15 functional genes and four pseudogenes (17, 26, 27, 29, 31, 50, 51, 53, 54, 57, 61, 63, 64, 65). It has been uncertain whether or not some of the cloned human IFN-α genes and cDNAs with few nucleotide differences, such as the Hu-IFN-αA, Hu-IFN-α2 and Hu-IFN-α2(Arg) genes, are allelic variants or represent distinct genes.

To determine if these sequences do indeed represent separate genes or are instead polymorphic variants of a single gene, sequences representing only the Hu-IFN-αA, Hu-IFN-α2 and Hu-IFN-α2(Arg) genes were amplified by nested polymerase chain reaction (PCR) from human genomic DNAs of healthy consenting individuals. These sequences were then subcloned and examined by sequencing of individual clones. In addition, the DNAs were examined from KG-1 (80) and Namalwa (81) cell lines from which the Hu-IFN-αA and Hu-IFN-α2(Arg) cDNAs, respectively, were cloned.

MODES FOR CARRYING OUT INVENTION

Three oligodeoxynucleotides were prepared by the phosphoramidite method (82, 83) and purified (84). Primer I (5'-TGGGCTGTGATCTGCCTC-3') complementary to nucleotides 125 to 142 at the 5' end was used with Primer II (5'-CATGATTTCTGCTCTGACAACC-3')

complementary to nucleotides 552 to 573 at the 3' end to amplify the desired nucleotide sequences. The DNA, as amplified by the polymerase chain reaction (PCR) with this primer pair, was expected to represent sequences from most of the IFN-α gene family (79). This conserved PCR product was then used as template in a second amplification reaction with the same 3' oligonucleotide but with a 5' oligonucleotide specific for the human IFN-αA, IFN-α2 and IFN-α2(Arg) genes only (79). The second reaction produced a product of 430 bp when Primer III (5'-AACCCACAGCCTGGGTAG-3') complementary to nucleotides 144 to 161 was substituted for the Primer I. The 430 bp DNA was purified and cloned into the *Sma*I site of pBluescript-SK$^-$ (Stratagene, LaJolla, CA) as described (79, 85, 86).

DNA of the plasmids was prepared by the alkaline lysis miniprep procedure (86, 87) from 1 ml cultures grown overnight in LB medium containing 100 μg/ml ampicillin. The resultant DNA pellet was sequenced by the dideoxy chain termination procedure (79, 88, 89). The reactions were run on 6% polyacrylamide gels which were then dried and exposed to X-ray film overnight at room temperature with an intensifying screen.

Reverse transcriptase PCR (RT-PCR) was used to analyze the expression of the IFN-α subtypes αA, α2 and α2(Arg) in the KG-1 and Namalwa cell lines (90). RNA was isolated at 6 hours after induction from Sendai virus-induced KG-1 cells (60) and at 8 hours post induction from NDV-stimulated Namalwa cells (91, 92).

DNA was extracted from the human myeloblastoid cell line KG-1 and from the lymphoblastoid Namalwa cell line by a modification of the method of Pellicer *et al.* (93).

After obtaining informed consent, human genomic DNA was prepared from whole blood samples collected from normal, healthy individuals by ammonium acetate precipitation as described (79, 94).

METHODOLOGICAL BASIS FOR INVENTION

The DNA from 11 normal individuals was amplified by nested PCR then cloned and sequenced as described above. The number of sequences corresponding to the various human IFN-α species is shown in Table 1. It can be seen that neither the sequence for the αA gene nor the α2(Arg) gene was detected in any of the normal individuals examined in this study. As shown in Table 2, however, the αA sequence was detected in the DNA from the KG-1 cell line, but not in Namalwa cells; and the α2(Arg) sequence was detected in the DNA from the Namalwa cell line, but not in KG-1 cells.

TABLE 1

Frequency of Hu-IFN-αA, -α2 and α2(Arg) Clones From Normal Individuals

Interferon Variant	Number of Clones
IFN-α2	165
IFN-αA	0
IFN-α2(Arg)	0
Other[1]	36
Total	201

[1] Other refers to sequences which contained one or more mutations in an area unrelated to the αA and α2(Arg) specific differences. It should be noted that the frequency of mutations detected is in the range or slightly lower than that predicted from the combined error rates of Taq DNA polymerase and Sequenase DNA polymerase (95, 96). Previous analysis of IFN-α2 genes have been reported (97,98), but did not discern any differences in their representation in the DNA from normal individuals. Descriptions and abbreviations relevant to interferons are described in detail in several references (10-12, 61, 99, 100).

TABLE 2

Frequency of IFN-α Clones From KG-1 and Namalwa Cell Lines

Cells	IFN-α2	IFN-αA	IFN-α2(Arg)	Other	Total
KG-1 cells	15	10	0	16	41
Namalwa cells	22	0	13	2	37

Restriction endonuclease analysis to detect the IFN-αA gene was also performed on DNA from five of the individuals from whom clones had been sequenced and on DNA from seven additional people that were not examined by DNA sequencing. It was found that the restriction endonuclease analysis of the amplified DNA from all of these individuals showed no IFN-αA gene present (See Ref. 79, Fig. 2).

PREFERRED EMBODIMENT OF INVENTION

From the foregoing analysis, it can be concluded that in human DNA from a wide variety of humans only Hu-IFN-α2 is present. The species Hu-IFN-αA and Hu-IFN-α2(Arg), not present in the DNA of 11 normal individuals, apparently arose during the development of the disease and/or the establishment of the cell lines in culture. It is noteworthy that the expression of these alleles of Hu-IFN-α2 yields IFN-α species with high activity in a wide variety of assays (63, 68, 69, 101-115). The specific activities of all three of these IFN-α species are comparable. Furthermore, it has been reported that patients treated with Hu-IFN-αA produced a higher level of anti-interferon antibodies than patients treated with Hu-IFN-α2 or Hu-IFN-αn (Welferon: a preparation of mixed Hu-IFN-α species produced by induced Namalwa cells) (116-124). Some of the new interferons produced by the described

invention may be able to by-pass neutralization by the antibodies produced in patients treated with IFN-α preparations in current use. Such new IFN-α species should be able to be used to treat patients who have relapsed because of neutralization of the administered IFN-α species.

While the inventor has, for convenience, used Hu-IFN-α2 and its known variants for establishing his hypothesis of the existence of a class of super or tumor interferons, it will be apparent to those skilled in the art that the results extend to an entire class of such interferons, as well as other polypeptides. Illustrative of this conclusion is the extraordinary high percentage of variant forms of the IFN-α2 and αA genes in KG-1 cells -- i.e., 39% (16/41), much more than could be explained by experimental error, as shown in the column labeled "Other" of Table 2.

It will also be apparent that the method of the invention, as illustrated above for Hu-IFN-α2, can be applied to any protein. In the general case, a primer pair is chosen to encompass part or all of the nucleotide coding sequence with the use of DNA from tumor cells or from cultured cells as templates for the PCR. The PCR product is then cloned and sequenced. The amino acid sequence predicted by the nucleotide sequence so obtained is compared to the sequence of the protein in normal individuals. Proteins with amino acid sequences different from those proteins in normal individuals are then cloned in appropriate expression vectors (11, 12, 14, 17, 45, 53, 54, 57, 63, 69, 86, 103), produced, purified and characterized. Those with desirable activities are then developed for therapeutic use.

The origin of the tumor interferons or super interferons is unknown. Yet, it is clear that they are developed during the pathological process. It is believed that the cells producing these interferons have been selected during development and progress of the disease.

The presence of allelic forms of IFN-α2 in the KG-1 and Namalwa cells is most noteworthy. DNA from leukocytes from normal individuals did not contain these variants. Because both the KG-1 and Namalwa cells originated from patients with leukemia or lymphoma, it is believed that this alteration is an early change in progression of these diseases. Indeed, it has been reported that there are significant gross changes in restriction endonuclease digestion patterns for the IFN-α genes in acute leukemias (125, 126).

The disease mechanisms involved in developing malignant cells and selection of those cells produce a wide variety of genetic changes in the resultant tumor cells. In order for cancer cells to grow unfettered, to escape the normal controls and to metastasize, the usual regulatory network of the immune system, involving growth inhibitors as the interferons and growth factors and hormones, may be modified. The control of cell growth and nonmalignant behavior is a delicate balance of many regulatory factors, a few of which gone astray can alter the normal growth patterns. Although it has been reported that changes in the DNA of cancer cells occurs, the changes have been focussed on oncogenes and tumor suppressor genes that lead to the malignant phenotype. The inventor has provided data that the changes are more pervasive than expected, not merely those changes focussed on oncogenes and tumor suppressors. Furthermore, by genetic changes (mutations in DNA) and selection of tumor cells for aggressiveness, many alterations will be embodied in the final tumor cell population. The new proteins produced will have lower, the same or higher activities than the normal proteins. By identifying those modified proteins associated with changes in activity, it will be possible to identify those proteins with new and/or enhanced activities.

From an analysis of initial clones obtained from the KG1 cell line (53, 54, 63), it was shown that several abnormal interferons exist in this cell line (also see ref. 61 for list of IFN-α species). This is especially evident in that αB (not previously recognized as an abnormal interferon) has an insertion and compensating deletion making an abnormal protein that differs from Hu-IFN-α8, the normal counterpart. The presence of an insertion and a compensating deletion producing a normal sized molecule suggests some enormous selective pressures to produce these interferons. The fact that an insertion and a deletion would be incorporated into a molecule simply by random stochastic processes without external pressures is highly unlikely. Thus, these modified interferons are seen to represent an entire new family of molecules that have been developed under the pressure of enormous external forces to provide for the selection of these species.

With respect to the interferons produced by mechanisms to enhance or combat the disease process, some may indeed have unusual properties and may be more active than some of the interferons produced by normal cells. For example, since interferon is a growth inhibitory molecule, production of a new interferon that could down regulate the receptors for interferon in cells and help select for cells without interferon receptors or low levels of interferon receptors may enhance the disease process. Such interferons could also help select cells with an altered signal transduction mechanism, but normal receptor number. Thus, a cell producing spontaneously some interferon, could be expected to have initially a low level of receptors due to down regulation and its growth would likely be reduced. Nevertheless, during the multiplication of such cells, cells would be selected that would have low levels of receptors so that they could escape the inhibition of the endogenous interferon. The same would hold

for a wide variety of other molecules such as cytokines, lymphokines, tumor suppressors, growth factors, anti-growth factors, matrix molecules, hormones, angiogenic factors, clotting factors, etc., all molecules that can control growth and/or metastases in one manner or another.

The altered proteins described herein are found in tumor cells or cultured cells obtained from tumors. Furthermore, selection of cell-lines in culture can also produce some of the alterations as selection *in vivo*.

CLONING OF Hu-IFN-α001

A new interferon was amplified from the genomic DNA of KG-1 cells (ATCC CCL 246) based on the strategies outlined hereinbefore and by the procedures described herein and elsewhere (79). The primers used to amplify the genes are shown in Table 3. The 5' primer contains an *Apa*I site, and the 3' primer contains an *Xba*I site for cloning. The PCR reactions were carried out in 50 μl with 100 ng KG-1 template DNA, 100 ng of each primer (6431 and 6432), 0.2 mM of each dNTP, and 2.5 units of Taq DNA Polymerase for 30 cycles of 94°C 30 seconds, 50°C 30 seconds, 72°C 30 seconds in the Perkin Elmer model 9600 thermocycler. Products of the PCR amplification were cloned into the *Apa*I and *Xba*I sites of plasmid pBluescript II KS+ (Stratagene) and then transformed into competent *E. coli* strain DH5α cells. Competent cells were prepared in 12% PEG and 36% glycerol in Luria-Bertani medium (L-broth medium, 10 g tryptone, 5 g yeast extract, 10 g NaCl, pH 7.3) from Digene (Silver Spring, MD 20904, Cat. No. 3500-1002) as described (127). Plasmid DNA was isolated from 2.0 ml of overnight cultures grown at 37°C by a modified alkaline lysis procedure as reported (128). The size of the inserts was determined by digestion with

restriction endonucleases *Kpn*I and *Sac*I that flanked the cloning sites in the vector pBluescript. A total of 10 independent colonies were identified that contained a 700 base pair insert.

Table 3

Primers for PCR Amplification

Primer	Sequence	Length	Primer No.
5'	GCGGGCCCCAATGGCCYTGYCCTTT	25	6431
3'	GCTCTAGAAYTCATGAAAGYGTGA	24	6432

The sequence of the primers are given in the 5' to 3' direction. The "Y" represents a pyrimidine (T or C).

The DNA from one of the clones (plasmid pBS001) was sequenced in both directions. Automated DNA sequencing was performed on a Genesis 2000 Automated DNA Sequencer (DuPont, Wilmington, DE) with the primers shown in Table 4 by methods previously reported (86,88,89). All sequences were performed on both strands. Automated sequencing was carried out and the results were compiled to create a consensus sequence. The sequence determined from the T3 primer represents the 5' end of the insert; the T7- derived sequence represents the 3' end.

The sequence so determined is designated Hu-IFN-α001 and is shown in Fig. 1. The location of the *Alw*NI restriction endonuclease recognition site (5' CAGNNNCTG 3') that was used for the splicing of the Hu-IFN-α001 insert into the expression vector TGATG (129) is indicated in the figure by underlining. The signal peptide is shown as the 23 amino acids labeled -1 to -23. As seen in Fig. 1, the mature protein contains 166 amino acids.

Table 4

Primers used for Sequencing

Designation	Sequence	Primer No.	Position in Hu-IFN-α001	Direction
IFN-A1	CTTGAAGGACAGACATG	6942	157 - 172	F
IFN-A2	CTGTCCTCCATGAGATG	6941	233 - 249	F
IFN-A3	GGTCATTCAGCTGCTGG	6940	339 - 355	R
IFN-A4	TCCTCCTTCATCAGGGG	6939	397 - 413	R
T3	ATTAACCCTCACTAAAG	T3	Vector	F
T7	TAATACGACTCACTATA	T7	Vector	R

All primers are shown from 5' to 3' orientation. The column designated "Direction" represents the direction of sequencing with respect to the sequence of the Hu-IFN-α: "F" represents forward; "R" - reverse. Oligodeoxynucleotides were synthesized on an Applied Biosystem DNA synthesizer model 380B by the phosphoramidite method (83,130).

A comparison of the protein sequence with other human interferon alpha species (Hu-IFN-α) demonstrates that Hu-IFN-α001 is most closely related to Hu-IFN-αJ. That comparison is graphically depicted in Fig. 2. A summary of the known Hu-IFN-α sequences has been previously reported (61). There are a total of six amino acid changes compared to Hu-IFN-αJ. The data clearly demonstrate that this tumor derived Hu-IFN-α species is different from any other known Hu-IFN-α species previously reported. Furthermore. it would not have been possible to predict this specific sequence as the number of possible proteins with alterations in these six positions is 20^6 or 64,000,000. One of the amino acid changes is in the signal peptide sequence; the remaining five alternations are in the mature protein. It is also to be emphasized that the derived Hu-IFN-α species presented here is a natural interferon derived from tumor cells. It is not a synthetic construct prepared by simply mutating six positions.

Expression of the Hu-IFN-α001 gene was accomplished in two steps. The plasmid pBS001 was digested with restriction endonuclease *Kpn*I (5' end of Hu-IFN-α001 sequence). The *Kpn*I ends were made blunt by incubation with T4 DNA polymerase in the following reaction mixture: 1 μg of DNA; 33 mM Tris acetate, pH 7.9; 66 mM potassium acetate; 10 mM magnesium acetate; 0.5 mM dithiothreitol: 100 μg/ml BSA (bovine serum albumin): 2 mM of each of the four dNTPs; 5 units of T4 DNA polymerase (United States Biochemical Corp.); total volume of 18 μl. Incubation was performed for 5 minutes at 37°C to prepare the blunt ends. The plasmid DNA was then digested with *Xba*I (3' end of Hu-IFN-α001 sequence) to release the insert containing the Hu-IFN-α001 sequence. The DNA fragments were then purified as described (86). The TGATG vector was prepared by digestion with restriction endonuclease *Sac*I. followed by preparing blunt ends with T4 DNA polymerase as described above. and then digested with restriction endonuclease *Xba*I. The fragment containing the Hu-IFN-α001 insert was then ligated to the pTGATG expression vector (129). After ligation the DNA was transformed into competent *E. coli* DH5α cells. Colonies were analyzed by growing the cells as described above to isolate plasmid DNA. The plasmids were then digested with restriction endonucleases *Eco*RI and *Xba*I to determine the size of the insert. An expression vector for Hu-IFN-αJ was prepared as previously described for the expression plasmids for Hu-IFN-αB2 and Hu-IFN-αA/D (131).

The nucleotide sequences encoding Hu-IFN-αJ and Hu-IFN-α001 contain an *Alw*NI site in identical positions of the sequence (Fig. 3); and. as illustrated in Fig. 3, which shows the structure of the plasmid pHu-IFN-α001 containing the expression vector for Hu-IFN-α001, there is a second *Alw*NI site in the vector itself.

In addition, because the *Alw*NI recognition sites (CAGNNN^CTG) have three unspecified nucleotides (NNN) in the 3' overhang, the religations are specific and asymmetric. Accordingly, pTGATG vectors (129) encoding Hu-IFN-αJ and Hu-IFN-α001 were digested with restriction endonuclease *Alw*NI to isolate the large vector and Hu-IFN-α001 (3' end) fragments, respectively. The Hu-IFN-α001 fragment was then ligated into the vector fragment from plasmid pHu-IFN-αJ to yield the *E. coli* expression vector pHu-IFN-α001, as shown in Fig. 3, which was transfected into competent *E. coli* (DH5α) cells (86).

Plasmid pHu-IFN-α001 is deposited with the American Type Culture Collection (ATCC) at 12301 Parklawn Drive, Rockville, MD 20852: Accession number: _____; Deposit date June 7, 1994; and designated as plasmid pHu-IFN-α001 (*E. coli* DH5α/pHu-IFN-α001 as the host vector system).

The *E. coli* (DH5α) cells containing the expression vector pHu-IFN-α001 were grown in 875 ml of Medium A overnight at 30°C in one 2 liter flask with rotary shaking. Medium A consists of KH_2PO_4 (4.5 g/L), $Na_2HPO_4{\bullet}7H_2O$ (18.9 g/L), NH_4Cl (1.5 g/L), NaCl (0.75 g/L), glucose (15 g/L), casamino acids (7.5 g/L), $MgSO_4{\bullet}7H_2O$ (0.369 g/L), thiamine hydrochloride (0.0015 g/L), leucine (0.04 g/L), proline (0.04 g/L) and ampicillin (0.05 g/L) adjusted to pH 7.4. The overnight culture was used to inoculate 22.5 liters of Medium A in a fermentor. The *E. coli* containing the expression vector were grown at 30°C until the A_{550} reached 7.0 at which time the temperature was raised to 42°C. The cells were harvested 3 hrs after temperature induction at 42°C by centrifugation and cell pellets divided into 50 g portions prior to freezing at -80°C. The cells were stored at -80°C until used for preparation of interferon.

PURIFICATION OF Hu-IFN-α001

For purification of Hu-IFN-α001, frozen *E. coli* cell paste was thawed by suspension in 10 volumes of Buffer A (50 mM Tris•HCl, pH 8.0, 50 mM NaCl, 10 mM EDTA, 0.1 mM PMSF, phenylmethylsufonylfluoride). After the addition of egg white lysozyme (0.2 mg/ml) the suspension was sonicated four times with 30 second bursts while kept in an ice bath. then incubated at 23°C overnight while stirring vigorously to eliminate viscosity contributed by DNA. The suspension was centrifuged for 20 minutes at 12,000 rpm at 4°C. The pellet was resuspended again in 10 volumes of Buffer A with 1% Triton X-100. 50 mM EDTA and 0.5 M NaCl and incubated for at least 2 hours (2 - 16 hrs) at room temperature with shaking and then centrifuged for 20 min at 12.000 rpm at 4°C. Once again, the pellet was resuspended in 5 volumes of Buffer A with 0.5 M NaCl and incubated for 60 min at room temperature with shaking and then centrifuged for 20 min at 12,000 rpm at 4°C; the supernatant was discarded. The pellet was dispersed in 2 volumes of Buffer A in the presence of a mixture of oxidized/reduced forms of glutathione (0.2 mM/2.0 mM) and solid guanidine•HCl (2.5 times bacterial weight) was added and the solution was stirred at room temperature for 7 hours. After this. the mixture was diluted tenfold with Buffer A and allowed to stand overnight. Renaturation of the interferon was carried out by very slow addition of 7 M guanidine•HCl to 0.7 M. The refolding of Hu-IFN-α001 in solution takes more than 15 hours. Since Hu-IFN-α001 contains two disulfide bonds. this step involves slow oxidation of the protein during dilution from guanidine-containing solution. Then suspension was then centrifuged to remove debris. Solid $(NH_4)_2SO_4$ was added to the supernatant to a final concentration 1 M, and the solution. after clarification by centrifugation. was loaded at 5 ml/min onto a column (Pharmacia XK 26/20 #18-1000-72) packed with 100 ml of the sorbent

Phenyl-Toyopearl 650 S (20-50 μm) (Supelco, #8-14477: 100 g), previously equilibrated with 3-4 column volumes of Buffer B (50 mM Tris•HCl, pH 7.4, 0.5 M guanidine•HCl and 1 M $(NH_4)_2SO_4$. The column effluent was monitored at 280 nm. After loading, the column was washed with Buffer B until the A_{280} of the effluent returned to near baseline level and then was eluted sequentially with 2-3 column volumes of Buffer C (50 mM Tris•HCl, 0.5 M guanidine•HCl, 0.6 M $(NH_4)_2SO_4$) with which the Hu-IFN-α001 was eluted. Peak fractions showing maximum bands of Hu-IFN-α001 on SDS-polyacrylamide gel electrophoresis were pooled. The Phenyl-Toyopearl column was regenerated *in situ* with 100 ml 0.5 M NaOH and 1 M NaCl solution; and was stored in 0.01% sodium azide. Fractions with Hu-IFN-001 as measured by antiviral activity and/or gel electrophoresis were pooled and concentrated 10-fold with an Amicon Centriprep 10 concentrator. The solution was then diluted 3-fold with Buffer D (20 mM Tris•HCl. pH 8.0, 5% glycerol) and was loaded onto a FPLC monoQ HR 10/10 ion exchange column (Pharmacia # 17-0556-01) equilibrated with Buffer D. The column was washed with about 10 ml of Buffer D until the A_{280} reached baseline. Elution of Hu-IFN-α001 was accomplished with a linear gradient of Buffer D and Buffer E (Buffer D plus 1 M NaCl) at a flow rate of 1.5 ml/min from 0 to 100% Buffer E over 3 hours. The Hu-IFN-α001 was eluted at 0.15 M NaCl in a single peak. The fractions were pooled, analyzed by sodium dodecylsulfate (SDS) polyacrylamide gel electrophoresis and assayed for antiviral activity. From 6 g of bacterial pellet (wet weight), about 8-10 mg of purified Hu-IFN-α001 was obtained.

The purified protein was mixed with 15 μl of SDS sample buffer (0.5 M Tris•HCl. pH 6.8, 1% (v/v) β-mercaptoethanol, 1% (w/v) sodium dodecylsulfate (SDS), 12% (v/v) glycerol. 2 mM ethylenediaminetetraacetic acid (EDTA). bromphenol blue) in a total

volume of 35 μl. The solution was boiled for two minutes after which 25 μl was loaded onto a 12.5% polyacrylamide gel with a 4% polyacrylamide stacking gel. The separating gel was buffered in 0.3 M Tris•HCl, 0.08% SDS, 2 mM EDTA, pH 8.8. The stacking gel was in 0.065 M Tris•HCl, pH 6.8, and 0.05% SDS. The chamber buffer was 25 mM Tris•HCl, 0.1% SDS, 0.2 M glycine. Electrophoresis was carried out for 1 hour at 150 V, 20 mA in the BioRad miniproteian II apparatus (132). The gel was stained with Coomassie Blue R-250 (2.4%, w/v, Coomassie Blue in 45% methanol, 9%, v/v, acetic acid) for 1 hour at room temperature; and destained in 8% acetic acid. From SDS-polyacrylamide gel electrophoresis it was apparent that the purified Hu-IFN-α001 migrated with a M_r of 20,000 as shown in Fig. 4. As indicated in that figure, Hu-IFN-α001 was placed in lanes 1, 2 and 3 in amounts of 3 μg, 1.5 μg and 0.75 μg, respectively. The columns labeled M represent the molecular weight markers with the values in kilodaltons given to the left of each respective molecular weight marker. As can be seen, the Hu-IFN-α001 exhibited a slightly slower mobility than Hu-IFN-αJ on SDS-polyacrylamide gel electrophoresis (SDS PAGE, ref. 132).

Antiviral activity of Hu-IFN-α001 was assayed on bovine MDBK and human FS7 cells with vesicular stomatitis virus (VSV) (Table 5) as described previously (133). The antiviral units were determined with respect to the human IFN-αA international standard Gxa01-901-535. There was approximately equal antiviral activity on human and bovine cells (Table 5) as is seen with many Hu-IFN-α species (17,27,30,100,103,134).

Table 5

Antiviral Assay of Interferon

Sample	Interferon Titer (units/ml)		Ratio
	FS-7 Cells	MDBK Cells	(FS-7/MDBK)
α001	1 x 10^8	1 x 10^8	1.0

The interferon titer is given in units/mg as described (10-12,99,100,133,135) with respect to the international standard for human interferon alpha A Gxa01-901-535 from the National Institutes of Health. Vesicular stomatitis virus (VSV) was used as the challenge virus with human FS-7 and bovine MDBK cells. The ratio of the antiviral activity of the interferon on FS-7 to that on MDBK cells is given in the last column. The samples of Hu-IFN-α001 were prepared as described in the text. Protein was determined by the method of Bradford (136).

Herein has been described an entire new class of molecules designated as super proteins, proteins not present in normal cells, but present in the cells in various diseased states and a method for identifying, producing and expressing such molecules. Although the present embodiment of the invention has been described in detail, it should be understood that various changes, alterations and substitutions can be made therein without departing from the spirit and scope of the invention as defined by the appended claims.

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